

AMENDMENTS TO THE SPECIFICATION

Please replace paragraph [0087] of the present application with the following amended paragraph.

[0087] High-risk HPV genotypes

HPV-16 5'-GCTGCCATATCTACTTCAGA (SEQ ID NO. 1)

HPV-18 5'-GCTTCTACACAGTCTCCTGT (SEQ ID NO. 2)

HPV-31 5'-GTG CTG CAA TTG CAA ACA GT (SEQ ID NO. 3)

HPV-33 5'-ACACAAGTAACTAGTGACAG (SEQ ID NO. 4)

HPV-45 5'-TATGTGCCTCTACACAAAAT (SEQ ID NO. 5)

Please replace paragraph [0088] of the present application with the following amended paragraph.

[0088] Low-risk HPV genotypes

HPV-6 5'-GTG CAT CCG TAA CTA CAT CTT (SEQ ID NO. 6)

HPV-11 5'-GTG CAT CTG TGT CTA AAT CTG (SEQ ID NO. 7)

Please replace paragraph [0089] of the present application with the following amended paragraph.

[0089] The GP5+/6+ amplification primer set sequence is:

GP5+ 5'-TTT GTT ACT GTG GTA GAT ACT AC 3' (SEQ ID NO. 8)

Biotin-GP6+ 5'-GAA AAA TAA ACT GTA AAT CAT ATT C 3' (SEQ ID NO. 9)

Please replace paragraph [0090] of the present application with the following amended paragraph.

[0090] The MY09/11 amplification primer set sequence is:

Biotin-MY09 5'-CGT CCM ARR GGA WAC TGA TC (SEQ ID NO. 10)

MY11 5'-GCM CAG GGW CAT AAY AAT GG (SEQ ID NO. 11)

Please replace paragraph [0102] of the present application with the following amended paragraph.

[0102] Extension/sequencing primers:

16S Seq-primer 19b
GCTGGCACGTAGTTAGCCG (SEQ ID NO. 12)

16S Seq-primer 31b
GTTAGCCGGTGCTTCTTCTG (SEQ ID NO. 13)

Please replace paragraph [0103] of the present application with the following amended paragraph.

[0103] By using the above mentioned primers the sequence data below is not necessary to sequence or analyze. In one group 19 bases is not necessary to sequence (compared to conventional technology) and in the other group 31 bases is not necessary to sequence.

Here the sequences which could be skipped:

(1) GCTGGCACGTAGTTAGCCG (SEQ ID NO. 14)

(2) GCTGGCACGGAGTTAGCCGGTGCTTCTTCTG (SEQ ID NO. 15)

Example 6

Winning Read Length and Typing of Bacteria by
Pyrosequencing Technology